Jerome Hui

List of Publications by Year
in descending order

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90 papers	3,282 citations	159525 30 h-index	168321 53 g-index
96 all docs	96 docs citations	96 times ranked	3937 citing authors

#	Article	IF	Citations
1	Adaptation to deep-sea chemosynthetic environments as revealed by mussel genomes. Nature Ecology and Evolution, 2017, 1, 121.	3.4	250
2	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	2.6	221
3	MicroRNA evolution by arm switching. EMBO Reports, 2011, 12, 172-177.	2.0	199
4	Terpenes and Terpenoids in Plants: Interactions with Environment and Insects. International Journal of Molecular Sciences, 2020, 21, 7382.	1.8	172
5	Functional Shifts in Insect microRNA Evolution. Genome Biology and Evolution, 2010, 2, 686-696.	1.1	131
6	Vitellogenesis in the red crabCharybdis feriatus: Hepatopancreas-specific expression and farnesoic acid stimulation of vitellogenin gene expression. Molecular Reproduction and Development, 2005, 70, 288-300.	1.0	128
7	Ancestral whole-genome duplication in the marine chelicerate horseshoe crabs. Heredity, 2016, 116, 190-199.	1.2	114
8	Genomic Sequence and Experimental Tractability of a New Decapod Shrimp Model, Neocaridina denticulata. Marine Drugs, 2014, 12, 1419-1437.	2.2	77
9	Comparative genomic and phylogenetic analysis of vitellogenin and other large lipid transfer proteins in metazoans. FEBS Letters, 2010, 584, 1273-1278.	1.3	74
10	Identification of putative ecdysteroid and juvenile hormone pathway genes in the shrimp Neocaridina denticulata. General and Comparative Endocrinology, 2015, 214, 167-176.	0.8	74
11	Juvenile hormone and sesquiterpenoids in arthropods: Biosynthesis, signaling, and role of MicroRNA. Journal of Steroid Biochemistry and Molecular Biology, 2018, 184, 69-76.	1.2	69
12	Vitellogenesis in the Sand Shrimp, Metapenaeus ensis: The Contribution from the Hepatopancreas-Specific Vitellogenin Gene (MeVg2)1. Biology of Reproduction, 2004, 71, 863-870.	1.2	68
13	Evolution of Ecdysis and Metamorphosis in Arthropods: The Rise of Regulation of Juvenile Hormone. Integrative and Comparative Biology, 2015, 55, 878-890.	0.9	67
14	How did arthropod sesquiterpenoids and ecdysteroids arise? Comparison of hormonal pathway genes in non-insect arthropod genomes. Genome Biology and Evolution, 2015, 7, evv120.	1.1	64
15	A â€œDevelopmental Hourglassâ€•in Fungi. Molecular Biology and Evolution, 2015, 32, 1556-1566.	3.5	61
16	Rapid Change of Microbiota Diversity in the Gut but Not the Hepatopancreas During Gonadal Development of the New Shrimp Model Neocaridina denticulata. Marine Biotechnology, 2015, 17, 811-819.	1.1	61
17	Sex-Biased Expression of MicroRNAs in Schistosoma mansoni. PLoS Neglected Tropical Diseases, 2013, 7, e2402.	1.3	60
18	Equal contribution of hepatopancreas and ovary to the production of vitellogenin (PmVg1) transcripts in the tiger shrimp, Penaeus monodon. Aquaculture, 2006, 254, 666-674.	1.7	59

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19	Characterization of the putative farnesoic acid O-methyltransferase (LvFAMeT) cDNA from white shrimp, Litopenaeus vannamei: Evidence for its role in molting. Peptides, 2008, 29, 252-260.	1.2	59
20	Features of the ancestral bilaterian inferred from Platynereis dumerilii ParaHox genes. BMC Biology, 2009, 7, 43.	1.7	58
21	Evolution and functional divergence of enzymes involved in sesquiterpenoid hormone biosynthesis in crustaceans and insects. Peptides, 2010, 31, 451-455.	1.2	55
22	Characterization of vitellogenin in the shrimpMetapenaeus ensis: Expression studies and hormonal regulation ofMeVg1 transcription in vitro. Molecular Reproduction and Development, 2006, 73, 424-436.	1.0	53
23	Extensive Chordate and Annelid Macrosynteny Reveals Ancestral Homeobox Gene Organization. Molecular Biology and Evolution, 2012, 29, 157-165.	3.5	53
24	Cloning and expression study of the lobster (Homarus americanus) vitellogenin: Conservation in gene structure among decapods. General and Comparative Endocrinology, 2009, 160, 36-46.	0.8	52
25	Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. Nature Communications, 2020, 11, 3051.	5.8	47
26	De Novo Transcriptome Sequencing of the Snail Echinolittorina malaccana: Identification of Genes Responsive to Thermal Stress and Development of Genetic Markers for Population Studies. Marine Biotechnology, 2014, 16, 547-559.	1.1	43
27	Small RNAs in Plant Responses to Abiotic Stresses: Regulatory Roles and Study Methods. International Journal of Molecular Sciences, 2015, 16, 24532-24554.	1.8	42
28	<i>Neocaridina denticulata</i>: A Decapod Crustacean Model for Functional Genomics. Integrative and Comparative Biology, 2015, 55, 891-897.	0.9	37
29	Halloween genes in panarthropods and the evolution of the early moulting pathway in Ecdysozoa. Royal Society Open Science, 2018, 5, 180888.	1.1	36
30	Origin and Evolution of Yolk Proteins: Expansion and Functional Diversification of Large Lipid Transfer Protein Superfamily1. Biology of Reproduction, 2013, 88, 102.	1.2	35
31	Diversity of Insect Sesquiterpenoid Regulation. Frontiers in Genetics, 2020, 11, 1027.	1.1	35
32	The Nereid on the rise: Platynereis as a model system. EvoDevo, 2021, 12, 10.	1.3	34
33	Do cnidarians have a ParaHox cluster? Analysis of synteny around a <i>Nematostella</i> homeobox gene cluster. Evolution & Development, 2008, 10, 725-730.	1.1	33
34	Structure, evolution and function of the bi-directionally transcribed iab-4/iab-8 microRNA locus in arthropods. Nucleic Acids Research, 2013, 41, 3352-3361.	6.5	32
35	The Lophotrochozoan TGF-β signalling cassette - diversification and conservation in a key signalling pathway. International Journal of Developmental Biology, 2014, 58, 533-549.	0.3	32
36	Vitellogenesis in the Red Crab,Charybdis feriatus: Contributions from Small Vitellogenin Transcripts (CfVg) and Farnesoic Acid Stimulation of CfVg Expression. Annals of the New York Academy of Sciences, 2005, 1040, 74-79.	1.8	31

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37	Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. Communications Biology, 2021, 4, 83.	2.0	31
38	A Burst of miRNA Innovation in the Early Evolution of Butterflies and Moths. Molecular Biology and Evolution, 2015, 32, 1161-1174.	3.5	30
39	Discovery of microRNA-like RNAs during early fruiting body development in the model mushroom Coprinopsis cinerea. PLoS ONE, 2018, 13, e0198234.	1.1	28
40	Draft genome assemblies and predicted microRNA complements of the intertidal lophotrochozoans Patella vulgata (Mollusca, Patellogastropoda) and Spirobranchus (Pomatoceros) lamarcki (Annelida,) Tj ETQq0 0 0 rg BT /Overlock 10 Tf	0.4	27
41	Animal regeneration in the era of transcriptomics. Cellular and Molecular Life Sciences, 2021, 78, 3941-3956.	2.4	27
42	Neuropeptide and microRNA regulators of juvenile hormone production. General and Comparative Endocrinology, 2020, 295, 113507.	0.8	25
43	Reconstruction of ancient homeobox gene linkages inferred from a new high-quality assembly of the Hong Kong oyster (Magallana hongkongensis) genome. BMC Genomics, 2020, 21, 713.	1.2	24
44	Chromosomalâ€level reference genome of the incense tree <i>Aquilaria sinensis</i>. Molecular Ecology Resources, 2020, 20, 971-979.	2.2	24
45	miRNA-Mediated Interactions in and between Plants and Insects. International Journal of Molecular Sciences, 2018, 19, 3239.	1.8	23
46	Genome of the Rusty Millipede, Trigoniulus corallinus, Illuminates Diplopod, Myriapod, and Arthropod Evolution. Genome Biology and Evolution, 2015, 7, 1280-1295.	1.1	21
47	MicroRNAs regulate the sesquiterpenoid hormonal pathway in<i>Drosophila</i>and other arthropods. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20171827.	1.2	20
48	How are comparative genomics and the study of microRNAs changing our views on arthropod endocrinology and adaptations to the environment?. General and Comparative Endocrinology, 2013, 188, 16-22.	0.8	19
49	Millipede genomes reveal unique adaptations during myriapod evolution. PLoS Biology, 2020, 18, e3000636.	2.6	18
50	The phylogenetic utility and functional constraint of microRNA flanking sequences. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20142983.	1.2	17
51	The potential risk of Schistosoma mansoni transmission by the invasive freshwater snail Biomphalaria straminea in South China. PLoS Neglected Tropical Diseases, 2020, 14, e0008310.	1.3	14
52	PBDE-47 exposure causes gender specific effects on apoptosis and heat shock protein expression in marine medaka, Oryzias melastigma. Aquatic Toxicology, 2014, 147, 57-67.	1.9	13
53	A crustacean annotated transcriptome (CAT) database. BMC Genomics, 2020, 21, 32.	1.2	13
54	Differential microRNA expression, microRNA arm switching, and microRNA:long noncoding RNA interaction in response to salinity stress in soybean. BMC Genomics, 2022, 23, 65.	1.2	13

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55	Comparative Genomics Reveals Insights into the Divergent Evolution of Astigmatic Mites and Household Pest Adaptations. Molecular Biology and Evolution, 2022, 39, .	3.5	13
56	Distribution and current infection status of Biomphalaria straminea in Hong Kong. Parasites and Vectors, 2017, 10, 351.	1.0	12
57	Myriapod genomes reveal ancestral horizontal gene transfer and hormonal gene loss in millipedes. Nature Communications, 2022, 13, .	5.8	12
58	Duplication of the ribosomal gene cluster in the marine polychaete Platynereis dumerilii correlates with ITS polymorphism. Journal of the Marine Biological Association of the United Kingdom, 2007, 87, 443-449.	0.4	11
59	The Role of MicroRNAs in Drosophila Regulation of Insulin-Like Peptides and Ecdysteroid Signalling: Where Are We Now?. Advances in Insect Physiology, 2017, , 55-85.	1.1	11
60	Genome of the ramshorn snail Biomphalaria straminea-an obligate intermediate host of schistosomiasis.. GigaScience, 2022, 11, .	3.3	11
61	Hemolymph Proteomics and Gut Microbiota of Horseshoe Crabs Tachypleus tridentatus and Carcinoscorpius rotundicauda. Frontiers in Marine Science, 2020, 7, .	1.2	9
62	Proteomic Analysis of the Venom of Jellyfishes Rhopilema esculentum and Sanderia malayensis. Marine Drugs, 2020, 18, 655.	2.2	9
63	Chromosomal level genome of Ilex asprella and insight into antiviral triterpenoid pathway. Genomics, 2022, 114, 110366.	1.3	9
64	<scp><i>VIP</i></scp>Â<i><scp>B</scp>arcoding</i>: composition vectorâ€based software for rapid species identification based on <scp>DNA</scp> barcoding. Molecular Ecology Resources, 2014, 14, 871-881.	2.2	8
65	Annelids in evolutionary developmental biology and comparative genomics. Parasite, 2008, 15, 321-328.	0.8	7
66	Comparative transcriptomics across populations offers new insights into the evolution of thermal resistance in marine snails. Marine Biology, 2016, 163, 1.	0.7	7
67	Future Perspectives for Research on the Biosynthesis of Juvenile Hormones and Related Sesquiterpenoids in Arthropod Endocrinology and Ecotoxicology. QSAR in Environmental and Health Sciences, 2013, , 15-30.	0.3	6
68	Transcriptomic and proteomic analyses of venom glands from scorpions Liocheles australasiae, Mesobuthus martensii, and Scorpio maurus palmatus. Peptides, 2021, 146, 170643.	1.2	6
69	Rethinking Sesquiterpenoids: A Widespread Hormone in Animals. International Journal of Molecular Sciences, 2022, 23, 5998.	1.8	5
70	Genome of the four-finger threadfin Eleutheronema tetradactylum (Perciforms: Polynemidae). BMC Genomics, 2020, 21, 726.	1.2	4
71	Single-Cell Atlas of the Drosophila Leg Disc Identifies a Long Non-Coding RNA in Late Development. International Journal of Molecular Sciences, 2022, 23, 6796.	1.8	4
72	Infection patterns of dengue, Zika and endosymbiont Wolbachia in the mosquito Aedes albopictus in Hong Kong. Parasites and Vectors, 2020, 13, 361.	1.0	3

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73	Small <scp>RNAs</scp> in Cnidaria: A review. Evolutionary Applications, 0, , .	1.5	3
74	Copepod incompatibilities. Nature Ecology and Evolution, 2018, 2, 1203-1204.	3.4	2
75	Micro-RNA Clusters Integrate Evolutionary Constraints on Expression and Target Affinities: The miR-6/5/4/286/3/309 Cluster in Drosophila. Molecular Biology and Evolution, 2020, 37, 2955-2965.	3.5	2
76	Characterisation of the Complete Chloroplast Genomes of Seven Hyacinthus orientalis L. Cultivars: Insights into Cultivar Phylogeny. Horticulturae, 2022, 8, 453.	1.2	2
77	Evolution and intelligent design in Hong Kong. Nature, 2009, 458, 571-571.	13.7	1
78	Isolation and Characterization of Polymorphic Microsatellite Loci for and Transferability Across Eight Confamilial Species (Atyidae, Decapoda). Zoological Studies, 2018, 57, e19.	0.3	1
79	Population Genomics, Transcriptional Response to Heat Shock, and Gut Microbiota of the Hong Kong Oyster Magallana hongkongensis. Journal of Marine Science and Engineering, 2022, 10, 237.	1.2	1
80	Pursuing greener farming by clarifying legume-insect pest interactions and developing marker-assisted molecular breeding. Advances in Botanical Research, 2022, , 211-258.	0.5	1
81	International symposium for comparative endocrinology and genomics in arthropods. General and Comparative Endocrinology, 2020, 299, 113622.	0.8	0
82	Tertiary Education of Evolutionary Biology in Asia. , 2015, , 81-86.		0
83	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
84	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
85	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
86	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
87	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
88	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
89	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
90	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0